

STN Search Summary 10/620,487

=> d his

(FILE 'HOME' ENTERED AT 13:19:23 ON 25 JAN 2005)

FILE 'CAPLUS' ENTERED AT 13:21:04 ON 25 JAN 2005

L1 6 S YFIK
L2 134 S s (RhtB or ydeD or yedA or lyseE or pecm or thrE) (s) (increas? or ehanc?)
L3 24 S L2 (S) (ACTIVIT? OR EXPRESSI? OR (COPY W NUMBER))
L4 2 S L3 (P) (MICROORGANSIM? OR COLI? OR ESCHERICHIA? OR BACTERI?)
L5 2 s L3 (p) (microorgansim? or coli? or escherichia? or bacteri? or yeast or fungus or enterobacteriaceae)
L6 3 s l3 and (phosphoglycerate or ?serine? or ?cysteine? or ?cystine? or ?glycine) and fermentati?

s l3 and (phosphoglycerate or ?serine? or ?cysteine? or ?cystine? or ?glycine) and fermentati?

=> s yfiK

L1 6 YFIK

=> d l1 1-6

x L1 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:131333 CAPLUS
DN 140:248969
TI High level cell-free expression and specific labeling of integral membrane proteins
AU Klammt, Christian; Loehr, Frank; Schaefer, Birgit; Haase, Winfried; Doetsch, Volker; Rueterjans, Heinz; Glaubitz, Clemens; Bernhard, Frank
CS Centre for Biomolecular Magnetic Resonance, Institute for Biophysical Chemistry, University of Frankfurt/Main, Frankfurt/Main, Germany
SO European Journal of Biochemistry (2004), 271(3), 568-580
CODEN: EJBCAI; ISSN: 0014-2956
PB Blackwell Publishing Ltd.
DT Journal
LA English
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

Appl L1 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:55470 CAPLUS
DN 140:127258
TI Fermentative production of amino acids of the phosphoglycerate family by Escherichia coli overexpressing gene yfiK
IN Maier, Thomas
PA Consortium fuer Elektrochemische Industrie GmbH, Germany
SO Eur. Pat. Appl., 16 pp.
CODEN: EPXXDW
DT Patent
LA German
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1382684	A1	20040121	EP 2003-15546	20030710
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
	DE 10232930	A1	20040205	DE 2002-10232930	20020719
	US 2004038352	A1	20040226	US 2003-620487	20030716
	CA 2433485	AA	20040119	CA 2003-2433485	20030717
	JP 2004049237	A2	20040219	JP 2003-199397	20030718
	CN 1487079	A	20040407	CN 2003-178667	20030718
PRAI	DE 2002-10232930	A	20020719		
RE.CNT	5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT				

* L1 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2003:116387 CAPLUS
DN 138:334174
TI YfiK from Escherichia coli promotes export of O-acetylserine and cysteine
AU Franke, Isabel; Resch, Armin; Dassler, Tobias; Maier, Thomas; Bock, August
CS Department Biologie I, Mikrobiologie, Universitat Munchen, Munich, Germany
SO Journal of Bacteriology (2003), 185(4), 1161-1166
CODEN: JOBAAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

X L1 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2001:880292 CAPLUS
DN 136:336109
TI Comprehensive DNA microarray analysis of Bacillus subtilis two-component regulatory systems
AU Kobayashi, Kazuo; Ogura, Mitsuo; Yamaguchi, Hirotake; Yoshida, Ken-Ichi; Ogasawara, Naotake; Tanaka, Teruo; Fujita, Yasutaro
CS Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, 630-0101, Japan
SO Journal of Bacteriology (2001), 183(24), 7365-7370
CODEN: JOBAAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

* L1 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2000:456755 CAPLUS
DN 133:85119
TI Production of L-amino acids by bacterium transformed with amino acid excretion protein homologs
IN Livshits, Vitaliy Arkadievich; Zakataeva, Natalia Pavlovna; Nakanishi, Kazuo; Aleshin, Vladimir Veniaminovich; Troshin, Petr Vladimirovich; Tokhmakova, Irina Lyvovna
PA Ajinomoto Co., Inc., Japan
SO Eur. Pat. Appl., 29 pp.
CODEN: EPXXDW

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	EP 1016710	A2	20000705	EP 1999-125263	19991217
	EP 1016710	A3	20000906		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	RU 2175351	C2	20011027	RU 1999-104431	19990309
	AU 9964493	A1	20000706	AU 1999-64493	19991213
	AU 764189	B2	20030814		
	ZA 9907767	A	20000630	ZA 1999-7767	19991220
	JP 2000189180	A2	20000711	JP 1999-373651	19991228
	BR 9906287	A	20010123	BR 1999-6287	19991228
	KR 2000048465	A	20000725	KR 1999-64627	19991229
	CN 1261626	A	20000802	CN 1999-127522	19991230
PRAI	RU 1998-124016	A	19981230		
	RU 1999-104431	A	19990309		

L1 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN

AN 1996:737199 CAPLUS

DN 126:100025

TI The Bacillus subtilis chromosome region near 78° contains the genes
encoding a new two-component system, three ABC transporters and a lipase

AU Yamamoto, Hiroki; Uchiyama, Shigeki; Sekiguchi, Junichi

CS Department of Applied Biology, Faculty of Textile Science, Technology,
Shinshu University, 3-15-1 Tokida, Ueda-shi, Nagano, 386, Japan

SO Gene (1996), 181(1/2), 147-151

CODEN: GENED6; ISSN: 0378-1119

PB Elsevier

DT Journal

LA English

=> d 14

L4 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2003:417877 CAPLUS

DN 139:2051

TI Over expressing E. coli yedA gene for
increase the yield of producing of L-amino acid and its
derivatives

IN Livshits, Vitaliy Arkadyevich; Vitushkina, Maria Viacheslavovna;
Gusyatiner, Mikhail Markovich; Ziyatdinov, Mikhail Kharisovich;
Akhverdian, Valery Zavenovich; Savrasova, Ekaterina Alekseevna;
Doroshenko, Vera Georgievna; Mashko, Sergey Vladimirovich

PA Ajinomoto Co., Inc., Japan

SO PCT Int. Appl., 28 pp.

CODEN: PIXXD2

DT Patent

LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003044191	A1	20030530	WO 2002-JP12202	20021121
	W: AU, BR, BY, CA, CN, HU, IL, IN, JP, KR, MX, NO, PL, UA, VN, ZA				
	RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT,				
	LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,				
	GW, ML, MR, NE, SN, TD, TG				
	RU 2229513	C2	20040527	RU 2001-131570	20011123
	EP 1449917	A1	20040825	EP 2002-788635	20021121
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				
	IE, FI, CY, TR, BG, CZ, EE, SK				
	US 2003148473	A1	20030807	US 2002-302983	20021125
PRAI	RU 2001-131570	A	20011123		
	WO 2002-JP12202	W	20021121		

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d 14 2

L4 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2003:266869 CAPLUS

DN 138:266848

TI Arginine repressor deficient strain of Escherichia or coryneform bacteria
with LysE gene overexpression for L-arginine production

IN Yamaguchi, Mikiko; Ito, Hisao; Gunji, Yoshiya; Yasueda, Hisashi

PA Ajinomoto Co., Inc., Japan

SO Jpn. Kokai Tokkyo Koho, 36 pp.

CODEN: JKXXAF

DT Patent

LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2003102490	A2	20030408	JP 2002-214736	20020724
	US 2003113899	A1	20030619	US 2002-196232	20020717
	CN 1398964	A	20030226	CN 2002-126904	20020725
PRAI	JP 2001-224586	A	20010725		

=> d 13 1

L3 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:133959 CAPLUS
DN 140:180654
TI Sulfur-containing animal feed additives from fermentation liquors from
microorganisms expressing genes for biosynthesis of sulfur amino acids and
derivatives
IN Buchholz, Michael; Binder, Michael; Hermann, Thomas; Pfefferle, Walter;
Thierbach, Georg
PA Degussa AG, Germany
SO Eur. Pat. Appl., 22 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	EP 1389427	A1	20040218	EP 2003-17146	20030729
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
	DE 10237479	A1	20040226	DE 2002-10237479	20020816
PRAI	DE 2002-10237479	A	20020816		

=> d abs 13

L3 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2005 ACS on STN
AB The invention relates to sulfur-containing animal-feed additives such as
cysteine, cystine and thiazolidines and their salts produced from fermentation
liquors, and to processes for their production The compds. are manufactured
by
microorganisms expressing genes for enzymes of biosynthesis of these
compds. at high levels. Use of a high-level expression
construct for the ydeD gene to increase the content of
L-cystine and thiazolidines is demonstrated.

=> 13 and (phosphoglycerate or ?serine? or ?cysteine? or ?cystine? or ?glycine) and
fermentati?

L3 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.

For a list of commands available to you in the current file, enter

"HELP COMMANDS" at an arrow prompt (=>).

=> d 16 1-3

X
L6 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:133959 CAPLUS
DN 140:180654
TI Sulfur-containing animal feed additives from fermentation
liquors from microorganisms expressing genes for biosynthesis of sulfur
amino acids and derivatives
IN Buchholz, Michael; Binder, Michael; Hermann, Thomas; Pfefferle, Walter;
Thierbach, Georg
PA Degussa AG, Germany
SO Eur. Pat. Appl., 22 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1389427	A1	20040218	EP 2003-17146	20030729
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
	DE 10237479	A1	20040226	DE 2002-10237479	20020816
PRAI	DE 2002-10237479	A	20020816		

L6 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:522540 CAPLUS
DN 137:89444
TI Use of ptsH gene of Corynebacterium glutamicum for L-lysine biosynthesis
IN Farwick, Mike; Mockel, Bettina; Pfefferle, Walter
PA Degussa AG, Germany
SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 755,187.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002090700	A1	20020711	US 2001-819930	20010329
	US 2003224499	A9	20031204		
	US 6818432	B2	20041116		
	DE 10001101	A1	20010719	DE 2000-10001101	20000113
	US 2002094554	A1	20020718	US 2001-755187	20010108
	US 2004005675	A9	20040108		
	US 2005009143	A1	20050113	US 2004-916437	20040812
PRAI	DE 2000-10001101	A	20000113		
	US 2000-503189	B2	20000214		
	US 2001-755187	A2	20010108		
	US 2001-819930	A3	20010329		

L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN
 AN 2001:867953 CAPLUS
 DN 136:19157
 TI The thrE gene of Corynebacterium glutamicum and its use in increasing
 yields of threonine in fermentation
 IN Rieping, Mechthild
 PA Degussa AG, Germany
 SO Ger. Offen., 24 pp.
 CODEN: GWXXBX
 DT Patent
 LA German
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 10102823	A1	20011129	DE 2001-10102823	20010123
	CA 2400777	AA	20011206	CA 2001-2400777	20010406
	WO 2001092545	A1	20011206	WO 2001-EP3980	20010406
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				
	CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,				
	HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,				
	LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,				
	SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,				
	ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,				
	DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,				
	BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP	1285075	A1	20030226	EP 2001-931575	20010406
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				
	IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US	2002155551	A1	20021024	US 2001-834721	20010416
PRAI	DE 2000-10026494	A1	20000527		
	US 2000-229328P	P	20000901		
	DE 2001-10102823	A	20010123		
	WO 2001-EP3980	W	20010406		

SEQUENCE SEARCH SUMMARY

10/620,487

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 10:50:19 ; Search time 3519 Seconds
(without alignments)
10078.794 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750	100.0	750	6 CQ759947	Appl EPPat 3/04 CQ759947 Sequence
2	750	100.0	10272	1 ECORBAB	Nash 1992? D13169 E.coli gene
3	750	100.0	16446	1 D90886	Yamamoto 1997 D90886 E.coli geno

	4	750	100.0	29254	1	ECOK12RIII		D64044 Escherichia
	5	750	100.0	110000	1	U00096_27		Continuation (28 o
	6	745.2	99.4	12322	1	AE015279		AE015279 Shigella
	7	745.2	99.4	290380	1	AE016987		AE016987 Shigella
	8	738.8	98.5	300099	1	AE016764		AE016764 Escherich
	9	687.6	91.7	12337	1	AE005488		AE005488 Escherich
	10	687.6	91.7	270365	1	AP002562		AP002562 Escherich
	11	588	78.4	588	6	E49391		E49391 Process for
	12	588	78.4	588	6	AX030083		AX030083 Sequence
	13	461.2	61.5	145050	1	AL627275		AL627275 Salmonell
c	14	461.2	61.5	300431	1	AE016835		AE016835 Salmonell
	15	458	61.1	21722	1	AE008820		AE008820 Salmonell
	16	265.8	35.4	618	6	AR388761		AR388761 Sequence
c	17	224.4	29.9	23738	2	AC020828		AC020828 Mus muscu
	18	156	20.8	372	6	AR388768		AR388768 Sequence
	19	100	13.3	100	6	AX999538		AX999538 Sequence
	20	100	13.3	100	6	AX999539		AX999539 Sequence
	21	100	13.3	100	6	AX999540		AX999540 Sequence
c	22	70.4	9.4	288404	1	AE017272		AE017272 Bacillus
c	23	63.8	8.5	302451	1	AE016812		AE016812 Vibrio vu
c	24	55.2	7.4	110000	1	AE017225_22		Continuation (23 o
c	25	55.2	7.4	110000	1	AE017334_22		Continuation (23 o
c	26	55.2	7.4	110000	1	AE017355_23		Continuation (24 o
c	27	55.2	7.4	293264	1	AE017031		AE017031 Bacillus
c	28	51	6.8	249500	1	AP005344		AP005344 Vibrio vu
	29	50.4	6.7	573	6	AX432019		AX432019 Sequence
c	30	49.6	6.6	300600	1	AP005084		AP005084 Vibrio pa
c	31	49	6.5	110000	1	BX950851_45		Continuation (46 o
	32	48.8	6.5	344805	1	BX640434		BX640434 Bordetell
	33	48.8	6.5	346287	1	BX640450		BX640450 Bordetell
c	34	47.8	6.4	304262	1	AE017005		AE017005 Bacillus
c	35	47.2	6.3	13848	1	AE004249		AE004249 Vibrio ch
	36	47.2	6.3	348171	1	BX640412		BX640412 Bordetell
c	37	44.4	5.9	310029	1	AE016868		AE016868 Pseudomon
c	38	42.8	5.7	142350	5	BX088596		BX088596 Zebrafish
c	39	42.8	5.7	278779	2	BX323579		BX323579 Danio rer
	40	42	5.6	669	6	AR319795		AR319795 Sequence
	41	41.4	5.5	301214	1	AE016786		AE016786 Pseudomon
	42	41	5.5	618	12	AY657639		AY657639 Synthetic
c	43	41	5.5	11869	1	AE004657		AE004657 Pseudomon
c	44	40.6	5.4	125020	9	AF429315		AF429315 Homo sapi
	45	40.4	5.4	14305	1	AE014000		AE014000 Yersinia

Yu 1995
16/2004
2001 Tin

GenCore version 5.1.6
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	750	100.0	750	12 ADK66005	Adk66005 E coli yf
2	588	78.4	588	3 AAA52690	Aaa52690 Escherich
3	295.8	39.4	1668	5 AAS81979	Aas81979 DNA encod
4	265.8	35.4	618	11 ACH99695	Ach99695 Klebsiell
5	156	20.8	372	11 ACH99702	Ach99702 Klebsiell

PD 04 April
EP PD=7100
WO PD=3/01
X

	6	100	13.3	100	8	ACD79726	Acd79726 E. coli K
	7	100	13.3	100	8	ACD79725	Acd79725 E. coli K
	8	100	13.3	100	8	ACD79727	Acd79727 E. coli K
	9	50.4	6.7	573	6	ABK73143	Abk73143 Bacillus
	10	42.6	5.7	2325	5	AAS92926	Aas92926 DNA encod
c	11	42.6	5.7	3020	5	AAS88917	Aas88917 DNA encod
	12	42	5.6	669	9	ADA31058	Ada31058 DNA encod
	13	39.8	5.3	636	10	ADF02251	Adf02251 Bacterial
	14	39.6	5.3	750	11	ABD10542	Abd10542 Pseudomon
	15	39	5.2	247682	12	ADL08109	Adl08109 Human gen
	16	38.2	5.1	636	11	ACH97476	Ach97476 Klebsiell
	17	37.2	5.0	609	10	ACF70009	Acf70009 Photorhab
c	18	37.2	5.0	110000	10	ACF65385_1	Continuation (2 of
c	19	37.2	5.0	110000	10	ACF67367_30	Continuation (31 o
	20	36.4	4.9	2000	8	ADA71938	Ada71938 Rice gene
c	21	35.6	4.7	492	10	ACD96860	Acd96860 Human col
	22	35.6	4.7	612	10	ACF71507	Acf71507 Photorhab
	23	35.6	4.7	110000	10	ACF67367_46	Continuation (47 o
c	24	35.6	4.7	110000	10	ACF65388_01	Continuation (2 of
	25	35.2	4.7	474	12	ADI45188	Adi45188 Rice isop
	26	35.2	4.7	1302	4	ABL21095	Abl21095 Drosophil
c	27	35.2	4.7	79467	9	ADA02717	Ada02717 Mouse Nfa
c	28	35.2	4.7	79467	10	ADB72455	Adb72455 Mouse Nfa
c	29	35.2	4.7	79467	10	ADE95965	Ade95965 Mouse Nfa
c	30	35	4.7	1877	4	ABL14601	Abl14601 Drosophil
c	31	35	4.7	4532	4	ABL14600	Abl14600 Drosophil
c	32	34.6	4.6	214	3	ADF57362	Adf57362 Urogenita
c	33	34.6	4.6	3821	5	ADL62643	Adl62643 Human ova
c	34	34.6	4.6	3825	5	ABV25634	Abv25634 Human pro
c	35	34.4	4.6	6996	4	ABL21622	Abl21622 Drosophil
	36	34.2	4.6	592	6	ABT11039	Abt11039 Human bre
	37	34.2	4.6	645	11	ACH96827	Ach96827 Klebsiell
	38	34.2	4.6	1707	6	AAS15596	Aas15596 DNA encod
c	39	34.2	4.6	2000	8	ADA71938	Ada71938 Rice gene
c	40	34.2	4.6	2000	12	ADJ41214	Adj41214 Plant cDN
	41	33.4	4.5	202	3	AAC25780	Aac25780 Human sec
c	42	33.4	4.5	1055	3	AAA07254	Aaa07254 Asparagin
c	43	33.4	4.5	3077	3	AAA07255	Aaa07255 Asparagin
c	44	33.4	4.5	9951	6	ABK39929	Abk39929 Human che
	45	33.4	4.5	29000	10	ADA66458	Ada66458 Human Tra

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 11:25:37 ; Search time 100 Seconds
(without alignments)
5330.917 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
Sequence: 1 gatccataaccccaaacta.....ttagtaacttgctacttaag 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length	Length			
1	265.8	35.4	618	4	US-09-489-039A-5490	X	Sequence 5490, Ap
2	156	20.8	372	4	US-09-489-039A-5497		Sequence 5497, Ap
3	42	5.6	669	4	US-09-328-352-2345		Sequence 2345, Ap
4	39.8	5.3	636	4	US-09-543-681A-2536		Sequence 2536, Ap
5	39.6	5.3	750	4	US-09-252-991A-9146		Sequence 9146, Ap
6	38.2	5.1	636	4	US-09-489-039A-3271		Sequence 3271, Ap
7	34.2	4.6	645	4	US-09-489-039A-2622		Sequence 2622, Ap
8	33.4	4.5	202	4	US-09-513-999C-29855		Sequence 29855, A
c 9	33.4	4.5	1055	3	US-09-410-028-1		Sequence 1, Appli
c 10	33.4	4.5	3077	3	US-09-410-028-3		Sequence 3, Appli
11	33	4.4	72604	3	US-09-268-992-7		Sequence 7, Appli

	12	33	4.4	72604	3	US-09-657-474-7	Sequence 7, Appli
c	13	32.8	4.4	1194	4	US-09-252-991A-9124	Sequence 9124, Ap
c	14	32.8	4.4	1326	4	US-09-252-991A-9206	Sequence 9206, Ap
	15	32.8	4.4	1329	4	US-09-252-991A-8853	Sequence 8853, Ap
	16	32.6	4.3	505	4	US-09-621-976-15639	Sequence 15639, A
c	17	32.2	4.3	1001	4	US-09-641-638-340	Sequence 340, App
c	18	32.2	4.3	1001	4	US-10-170-097-340	Sequence 340, App
	19	32.2	4.3	5127	4	US-09-462-606-1	Sequence 1, Appli
	20	32.2	4.3	7207	4	US-09-462-606-3	Sequence 3, Appli
c	21	32	4.3	1338	4	US-09-489-039A-6698	Sequence 6698, Ap
c	22	31.8	4.2	789	4	US-09-134-000C-2827	Sequence 2827, Ap
c	23	31.4	4.2	965	4	US-09-270-767-14185	Sequence 14185, A
	24	31.2	4.2	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	25	30.8	4.1	726	4	US-09-328-352-3033	Sequence 3033, Ap
c	26	30.8	4.1	936	4	US-09-489-039A-5469	Sequence 5469, Ap
	27	30.8	4.1	1040	4	US-09-602-787A-305	Sequence 305, App
c	28	30.8	4.1	1497	4	US-09-220-132-94	Sequence 94, Appl
	29	30.8	4.1	1500	4	US-09-602-787A-301	Sequence 301, App
	30	30.6	4.1	1269	4	US-09-489-039A-3734	Sequence 3734, Ap
	31	30.6	4.1	5396	4	US-09-270-767-29115	Sequence 29115, A
	32	30.6	4.1	7233	4	US-09-270-767-13200	Sequence 13200, A
c	33	30.4	4.1	1294	2	US-08-665-647-4	Sequence 4, Appli
c	34	30.4	4.1	1521	4	US-09-252-991A-6495	Sequence 6495, Ap
c	35	30.4	4.1	4599	4	US-09-302-626B-61	Sequence 61, Appl
c	36	30.4	4.1	5562	4	US-10-204-708-63	Sequence 63, Appl
	37	30.4	4.1	9018	4	US-10-220-587-3	Sequence 3, Appli
	38	30.2	4.0	636	4	US-09-489-039A-2437	Sequence 2437, Ap
c	39	30.2	4.0	854	4	US-09-302-626B-57	Sequence 57, Appl
c	40	30.2	4.0	5937	4	US-09-302-626B-59	Sequence 59, Appl
c	41	30.2	4.0	38564	4	US-09-734-673-3	Sequence 3, Appli
c	42	30	4.0	454	4	US-09-513-999C-10704	Sequence 10704, A
	43	30	4.0	832	4	US-09-621-976-2813	Sequence 2813, Ap
c	44	30	4.0	849	4	US-09-540-236-656	Sequence 656, App
	45	30	4.0	1173	4	US-09-248-796A-6337	Sequence 6337, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 10:05:31 ; Search time 520 Seconds
(without alignments)
8146.523 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
Sequence: 1 gatccataaccccaaaccta.....ttagtaacttgctacttaag 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	750	100.0	750	16	US-10-620-487-1	Sequence 1, Appli	
2	50.4	6.7	573	9	US-09-974-300-434	Sequence 434, App	
3	39	5.2	247682	16	US-10-235-192A-28	Sequence 28, Appl	
4	36.8	4.9	852	16	US-10-425-114-35996	Sequence 35996, A	
5	36.8	4.9	2727	18	US-10-425-115-65647	Sequence 65647, A	
c 6	36	4.8	486	17	US-10-767-795-2906	Sequence 2906, Ap	
7	35.2	4.7	474	16	US-10-259-194A-119	Sequence 119, App	
c 8	35.2	4.7	79467	16	US-10-052-482-223	Sequence 223, App	
c 9	34.6	4.6	214	9	US-09-933-797-681	Sequence 681, App	
c 10	34.6	4.6	3821	10	US-09-814-353-20855	Sequence 20855, A	
c 11	34.6	4.6	3825	18	US-10-357-930-25623	Sequence 25623, A	
c 12	34.4	4.6	6630	17	US-10-437-963-75212	Sequence 75212, A	
c 13	34.2	4.6	2000	16	US-10-260-238-2214	Sequence 2214, Ap	
c 14	34.2	4.6	141463	13	US-10-087-192-22	Sequence 22, Appl	
c 15	33.8	4.5	497	16	US-10-424-599-84060	Sequence 84060, A	
c 16	33.4	4.5	2924	16	US-10-424-599-28594	Sequence 28594, A	
c 17	33.4	4.5	9951	16	US-10-257-166-10	Sequence 10, Appl	
18	33.4	4.5	29000	10	US-09-906-158-17	Sequence 17, Appl	
19	33.4	4.5	29000	15	US-10-388-263-466	Sequence 466, App	
20	33.2	4.4	235	16	US-10-424-599-141309	Sequence 141309,	
21	33.2	4.4	826	16	US-10-424-599-97789	Sequence 97789, A	
22	33.2	4.4	3673778	15	US-10-312-841-2	Sequence 2, Appli	
23	33	4.4	72604	15	US-10-162-497-7	Sequence 7, Appli	
24	33	4.4	72604	17	US-10-629-313-7	Sequence 7, Appli	
25	32.8	4.4	64492	16	US-10-378-083-1	Sequence 1, Appli	
26	32.6	4.3	451	14	US-10-123-155-126	Sequence 126, App	
27	32.6	4.3	451	15	US-10-146-731-126	Sequence 126, App	
28	32.6	4.3	451	15	US-10-140-472-126	Sequence 126, App	
29	32.6	4.3	451	15	US-10-141-761-126	Sequence 126, App	
30	32.6	4.3	451	15	US-10-142-885-126	Sequence 126, App	
31	32.6	4.3	451	15	US-10-158-790-126	Sequence 126, App	
32	32.6	4.3	451	15	US-10-137-871-126	Sequence 126, App	
33	32.6	4.3	451	15	US-10-140-923-126	Sequence 126, App	
34	32.6	4.3	451	15	US-10-141-756-126	Sequence 126, App	
35	32.6	4.3	451	15	US-10-141-759-126	Sequence 126, App	
36	32.6	4.3	451	15	US-10-140-805-126	Sequence 126, App	
37	32.6	4.3	451	15	US-10-140-864-126	Sequence 126, App	
38	32.6	4.3	451	16	US-10-142-426-126	Sequence 126, App	
39	32.6	4.3	597	18	US-10-363-345A-13041	Sequence 13041, A	
c 40	32.6	4.3	597	18	US-10-363-345A-13042	Sequence 13042, A	
c 41	32.6	4.3	623	17	US-10-767-701-883	Sequence 883, App	
42	32.6	4.3	858	18	US-10-363-345A-21325	Sequence 21325, A	
c 43	32.6	4.3	858	18	US-10-363-345A-21326	Sequence 21326, A	
c 44	32.6	4.3	2589	18	US-10-425-115-175990	Sequence 175990,	
c 45	32.4	4.3	289	17	US-10-437-963-54974	Sequence 54974, A	

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2005, 11:23:52 ; Search time 3085 Seconds
(without alignments)
8858.930 Million cell updates/sec

Title: US-10-620-487-1
Perfect score: 750
Sequence: 1 gatccataaccccaaaccta.....ttagtaacttgctacttaag 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
c 1	473	63.1	681	6	CA366654	CA366654 642278 NC
2	351	46.8	856	9	CL650636	CL650636 PRI0110a_
3	331.4	44.2	791	9	CL688782	CL688782 PRI014b_G
4	321.6	42.9	736	9	CL688905	CL688905 PRI014d_C
c 5	113.2	15.1	118	6	CA374430	CA374430 648800 NC
c 6	55.2	7.4	819	8	BH447440	BH447440 BOHQB49TF
7	50	6.7	420	8	BH374397	BH374397 AG-ND-180
c 8	49.4	6.6	862	9	CL666889	CL666889 PRI0153c_

	9	43.4	5.8	450	8	BH379453	BH379453	AG-ND-163
c	10	39.2	5.2	938	9	CL139330	CL139330	ISB1-112E
c	11	38.2	5.1	474	9	AG240288	AG240288	Lotus cor
	12	38.2	5.1	1101	9	CNS00EEC	AL069085	Drosophil
c	13	37.6	5.0	553	5	BM965274	BM965274	kj93h10.y
c	14	37.6	5.0	568	5	BQ095448	BQ095448	kk05d05.y
c	15	37.6	5.0	583	5	BM965121	BM965121	kj92c03.y
c	16	37.6	5.0	623	5	BM965443	BM965443	kj95h06.y
c	17	37.6	5.0	637	5	BM965333	BM965333	kj94f01.y
c	18	37.4	5.0	493	9	CE114952	CE114952	tigr-gss-
	19	37.4	5.0	884	9	CNS006U0	AL065923	Drosophil
c	20	37.2	5.0	939	9	CNS00CNG	AL059400	Drosophil
	21	36.8	4.9	614	5	BQ628514	BQ628514	sap47h10.
	22	36.8	4.9	650	6	CD598566	CD598566	RK114A3B1
	23	36.8	4.9	650	6	CD599088	CD599088	RK114A4B0
c	24	36.8	4.9	712	9	BX163185	BX163185	Danio rer
	25	36.8	4.9	778	9	BX175544	BX175544	Danio rer
	26	36.6	4.9	408	8	BZ716786	BZ716786	OGEBE26TM
	27	36.6	4.9	589	9	CC604749	CC604749	OGUHO32TH
c	28	36.6	4.9	787	9	CNS016H3	AL106737	Drosophil
c	29	36.6	4.9	935	9	CC604756	CC604756	OGUHO32TV
	30	36.6	4.9	963	9	CG050339	CG050339	PUIIH51TB
	31	36.4	4.9	440	6	CA678514	CA678514	wlm12.pk0
c	32	36.4	4.9	566	6	CD347163	CD347163	EtESTef11
c	33	36.4	4.9	619	5	BM964489	BM964489	kj84e08.y
	34	36.2	4.8	825	9	CC534336	CC534336	CH240_412
c	35	36	4.8	630	5	BM964821	BM964821	kj88g02.y
c	36	36	4.8	688	8	BZ659718	BZ659718	OGCCC31TM
c	37	35.8	4.8	1181	9	AG127050	AG127050	Pan trogl
c	38	35.6	4.7	492	1	AI908572	AI908572	RC-BT177-
c	39	35.4	4.7	699	9	CE799079	CE799079	tigr-gss-
	40	35.4	4.7	733	8	BZ389118	BZ389118	EINDJ32TF
	41	35.4	4.7	792	9	CG872981	CG872981	ZMMBBc028
c	42	35.2	4.7	226	4	BG370992	BG370992	dac11a02.
	43	35.2	4.7	500	5	BP188868	BP188868	BP188868
	44	35.2	4.7	500	5	BP189161	BP189161	BP189161
c	45	35.2	4.7	552	9	BX163834	BX163834	Danio rer

P

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OM protein - protein search, using sw model

Run on: January 3, 2005, 07:57:25 ; Search time 81 Seconds
(without alignments)
863.608 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	996	100.0	195	8	ADK66006	Adk66006 E coli Yf
2	993	99.7	195	3	AAB01788	Aab01788 Escherich
3	684	68.7	205	7	ABO66144	Abo66144 Klebsiell
4	505	50.7	344	4	ABG17792	Abg17792 Novel hum
5	272.5	27.4	249	7	ABO76971	Abo76971 Pseudomon
6	256	25.7	203	6	ABM70439	Abm70439 Photorhab
7	250.5	25.2	211	7	ABO63925	Abo63925 Klebsiell
8	232.5	23.3	212	7	ADF04482	Adf04482 Bacterial
9	228.5	22.9	211	7	ADF06423	Adf06423 Bacterial

Appl
Livshits
bo
vaccine
x

10	191.5	19.2	238	6	ADA35835	Ada35835	Acinetoba
11	178	17.9	241	6	ADA35872	Ada35872	Acinetoba
12	173	17.4	271	7	ABO83709	Abo83709	Pseudomon
13	163.5	16.4	235	6	ADA36962	Ada36962	Acinetoba
14	162	16.3	214	7	ABO61549	Abo61549	Klebsiell
15	161.5	16.2	206	6	ABU32233	Abu32233	Protein e
16	158.5	15.9	206	7	ABO70000	Abo70000	Pseudomon
17	158.5	15.9	211	6	ABU39959	Abu39959	Protein e
18	157.5	15.8	190	4	ABG29208	Abg29208	Novel hum
19	157.5	15.8	206	6	ABU28287	Abu28287	Protein e
20	156.5	15.7	206	6	ABU50100	Abu50100	Protein e
21	156.5	15.7	206	6	ABU47858	Abu47858	Protein e
22	155.5	15.6	214	6	ADA34738	Ada34738	Acinetoba
23	155.5	15.6	237	7	ABO78429	Abo78429	Pseudomon
24	154	15.5	205	6	ABU44939	Abu44939	Protein e
25	154	15.5	210	6	ADA35521	Ada35521	Acinetoba
26	153.5	15.4	211	7	ABO72001	Abo72001	Pseudomon
27	153	15.4	214	7	ABO63276	Abo63276	Klebsiell
28	151.5	15.2	211	6	ABU19902	Abu19902	Protein e
29	149.5	15.0	250	7	ADF04202	Adf04202	Bacterial
30	148	14.9	211	7	ABO63091	Abo63091	Klebsiell
31	146.5	14.7	220	6	ADA33616	Ada33616	Acinetoba
32	146	14.7	222	6	ADA35184	Ada35184	Acinetoba
33	143.5	14.4	212	3	AAB01787	Aab01787	Escherich
34	138.5	13.9	219	7	ABO61214	Abo61214	Klebsiell
35	137.5	13.8	205	6	ABU49040	Abu49040	Protein e
36	132	13.3	208	6	ADA33824	Ada33824	Acinetoba
37	129	13.0	201	6	ABM68999	Abm68999	Phototrab
38	128.5	12.9	228	7	ADF04569	Adf04569	Bacterial
39	128.5	12.9	240	6	ADA36250	Ada36250	Acinetoba
40	128	12.9	220	7	ADF04260	Adf04260	Bacterial
41	127	12.8	200	6	ADA33486	Ada33486	Acinetoba
42	126	12.7	205	3	AAY79298	Aay79298	E. coli R
43	126	12.7	205	3	AAY99597	Aay99597	E. coli L
44	125.5	12.6	214	6	ADA35408	Ada35408	Acinetoba
45	123.5	12.4	209	6	ABU38890	Abu38890	Protein e

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OM protein - protein search, using sw model

Run on: January 3, 2005, 08:54:35 ; Search time 25 Seconds
(without alignments)
517.280 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	684	68.7	205	4	US-09-489-039A-12661	Sequence 12661, A
2	272.5	27.4	249	4	US-09-252-991A-25717	Sequence 25717, A
3	250.5	25.2	211	4	US-09-489-039A-10442	Sequence 10442, A
4	232.5	23.3	212	4	US-09-543-681A-4767	Sequence 4767, Ap
5	228.5	22.9	211	4	US-09-543-681A-6708	Sequence 6708, Ap
6	191.5	19.2	238	4	US-09-328-352-7122	Sequence 7122, Ap
7	178	17.9	241	4	US-09-328-352-7159	Sequence 7159, Ap
8	173	17.4	271	4	US-09-252-991A-32455	Sequence 32455, A
9	163.5	16.4	235	4	US-09-328-352-8249	Sequence 8249, Ap
10	162	16.3	214	4	US-09-489-039A-8066	Sequence 8066, Ap
11	158.5	15.9	206	4	US-09-252-991A-18746	Sequence 18746, A

12	155.5	15.6	214	4	US-09-328-352-6025	Sequence 6025, Ap
13	155.5	15.6	237	4	US-09-252-991A-27175	Sequence 27175, A
14	154	15.5	210	4	US-09-328-352-6808	Sequence 6808, Ap
15	153.5	15.4	211	4	US-09-252-991A-20747	Sequence 20747, A
16	153	15.4	214	4	US-09-489-039A-9793	Sequence 9793, Ap
17	149.5	15.0	250	4	US-09-543-681A-4487	Sequence 4487, Ap
18	148	14.9	211	4	US-09-489-039A-9608	Sequence 9608, Ap
19	146.5	14.7	220	4	US-09-328-352-4903	Sequence 4903, Ap
20	146	14.7	222	4	US-09-328-352-6471	Sequence 6471, Ap
21	138.5	13.9	219	4	US-09-489-039A-7731	Sequence 7731, Ap
22	132	13.3	208	4	US-09-328-352-5111	Sequence 5111, Ap
23	128.5	12.9	228	4	US-09-543-681A-4854	Sequence 4854, Ap
24	128.5	12.9	240	4	US-09-328-352-7537	Sequence 7537, Ap
25	128	12.9	220	4	US-09-543-681A-4545	Sequence 4545, Ap
26	127	12.8	200	4	US-09-328-352-4773	Sequence 4773, Ap
27	126	12.7	205	3	US-09-396-357-2	Sequence 2, Appli
28	125.5	12.6	214	4	US-09-328-352-6695	Sequence 6695, Ap
29	123.5	12.4	228	4	US-09-252-991A-23837	Sequence 23837, A
30	123.5	12.4	277	4	US-09-252-991A-23018	Sequence 23018, A
31	122.5	12.3	201	4	US-09-328-352-6409	Sequence 6409, Ap
32	115.5	11.6	260	4	US-09-252-991A-25992	Sequence 25992, A
33	112.5	11.3	249	4	US-09-328-352-5813	Sequence 5813, Ap
34	112	11.2	217	4	US-09-489-039A-8076	Sequence 8076, Ap
35	111.5	11.2	222	4	US-09-252-991A-26644	Sequence 26644, A
36	109.5	11.0	216	4	US-09-252-991A-18666	Sequence 18666, A
37	107.5	10.8	206	4	US-09-328-352-4784	Sequence 4784, Ap
38	105.5	10.6	209	4	US-09-328-352-8225	Sequence 8225, Ap
39	104.5	10.5	210	4	US-09-328-352-4775	Sequence 4775, Ap
40	103.5	10.4	226	4	US-09-252-991A-31610	Sequence 31610, A
41	102.5	10.3	221	4	US-09-328-352-6659	Sequence 6659, Ap
42	99	9.9	213	4	US-09-489-039A-11845	Sequence 11845, A
43	98.5	9.9	138	4	US-09-711-164-445	Sequence 445, App
44	98.5	9.9	269	4	US-09-489-039A-7320	Sequence 7320, Ap
45	97.5	9.8	450	4	US-09-252-991A-20484	Sequence 20484, A

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OM protein - protein search, using sw model

Run on: January 3, 2005, 08:41:11 ; Search time 444 Seconds
(without alignments)
157.989 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	996	100.0	195	15	US-10-620-487-2 <i>ADD</i>	Sequence 2, Appli
2	161.5	16.2	206	15	US-10-282-122A-60157	Sequence 60157, A
3	158.5	15.9	211	15	US-10-282-122A-67883	Sequence 67883, A
4	157.5	15.8	206	15	US-10-282-122A-56211	Sequence 56211, A
5	156.5	15.7	206	15	US-10-282-122A-75782	Sequence 75782, A
6	156.5	15.7	206	15	US-10-282-122A-78024	Sequence 78024, A
7	154	15.5	205	15	US-10-282-122A-72863	Sequence 72863, A
8	151.5	15.2	211	15	US-10-282-122A-47826	Sequence 47826, A
9	142	14.3	217	14	US-10-156-761-10918	Sequence 10918, A
10	137.5	13.8	205	15	US-10-282-122A-76964	Sequence 76964, A
11	126	12.7	205	9	US-09-927-395-2	Sequence 2, Appli
12	126	12.7	205	9	US-09-847-392-2	Sequence 2, Appli
13	123.5	12.4	209	15	US-10-282-122A-66814	Sequence 66814, A
14	120	12.0	181	15	US-10-282-122A-44873	Sequence 44873, A
15	117.5	11.8	210	15	US-10-282-122A-69338	Sequence 69338, A
16	116.5	11.7	223	9	US-09-738-626-6070	Sequence 6070, Ap
17	116.5	11.7	223	10	US-09-746-660A-14	Sequence 14, Appl
18	112	11.2	207	9	US-09-738-626-6418	Sequence 6418, Ap
19	112	11.2	227	15	US-10-461-194-124	Sequence 124, App
20	111	11.1	227	15	US-10-461-194-94	Sequence 94, Appl
21	110.5	11.1	205	14	US-10-156-761-11297	Sequence 11297, A
22	109.5	11.0	209	15	US-10-282-122A-51102	Sequence 51102, A
23	107.5	10.8	224	14	US-10-156-761-7796	Sequence 7796, Ap
24	104	10.4	226	9	US-09-738-626-3665	Sequence 3665, Ap
25	98.5	9.9	138	14	US-10-287-274-445	Sequence 445, App
26	98.5	9.9	138	15	US-10-282-122A-42680	Sequence 42680, A
27	96	9.6	948	16	US-10-437-963-161288	Sequence 161288,
28	95.5	9.6	473	15	US-10-282-122A-61289	Sequence 61289, A
29	95	9.5	537	15	US-10-282-122A-68111	Sequence 68111, A
30	93.5	9.4	212	15	US-10-374-903A-6	Sequence 6, Appli
31	92	9.2	486	14	US-10-369-493-15301	Sequence 15301, A
32	92	9.2	488	14	US-10-369-493-15667	Sequence 15667, A
33	92	9.2	488	14	US-10-369-493-16057	Sequence 16057, A
34	92	9.2	625	14	US-10-369-493-3850	Sequence 3850, Ap
35	91.5	9.2	264	11	US-09-864-408A-4810	Sequence 4810, Ap
36	91	9.1	246	15	US-10-424-599-253409	Sequence 253409,
37	91	9.1	470	16	US-10-767-701-44234	Sequence 44234, A
38	91	9.1	551	9	US-09-738-626-4431	Sequence 4431, Ap
39	91	9.1	551	15	US-10-627-476-510	Sequence 510, App
40	90.5	9.1	680	16	US-10-437-963-142247	Sequence 142247,
41	90	9.0	204	14	US-10-156-761-8429	Sequence 8429, Ap
42	90	9.0	468	15	US-10-282-122A-52688	Sequence 52688, A
43	90	9.0	552	15	US-10-282-122A-53662	Sequence 53662, A
44	89.5	9.0	754	15	US-10-282-122A-48878	Sequence 48878, A
45	88.5	8.9	536	11	US-09-809-665A-71	Sequence 71, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 09:05:56 ; Search time 4048 Seconds
(without alignments)
2278.036 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134449_9000/app_query.fasta_1.39
1

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487@cgn_1_1_3731@runat_29122004_134449_9000 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	996	100.0	588	6	E49391 JP 7/00	E49391 Process for ★
2	996	100.0	588	6	AX030083 Livshits 7/00	AX030083 Sequence
3	996	100.0	750	6	CQ759947 Appl	CQ759947 Sequence
4	996	100.0	10272	1	ECORBAB X	D13169 E.coli gene
5	996	100.0	16446	1	D90886 SEQ 1997 Yamamoto	D90886 E.coli geno
6	996	100.0	29254	1	ECOK12RIII SEQ M85 X	D64044 Escherichia
7	996	100.0	110000	1	U00096_27 SEQ X	Continuation (28 o
8	992	99.6	300099	1	AE016764 X "	AE016764 Escherich
9	990	99.4	12322	1	AE015279 X "	AE015279 Shigella
10	990	99.4	290380	1	AE016987 X "	AE016987 Shigella
11	982	98.6	12337	1	AE005488 X "	AE005488 Escherich
12	982	98.6	270365	1	AP002562 X "	AP002562 Escherich
13	887	89.1	21722	1	AE008820 Y	AE008820 Salmonell
14	887	89.1	145050	1	AL627275 Y	AL627275 Salmonell
c 15	887	89.1	300431	1	AE016835	AE016835 Salmonell
16	684	68.7	618	6	AR388761	AR388761 Sequence
c 17	311.5	31.3	110000	1	AE017225_22	Continuation (23 o
c 18	311.5	31.3	110000	1	AE017334_22	Continuation (23 o
c 19	311.5	31.3	110000	1	AE017355_23	Continuation (24 o
c 20	311.5	31.3	293264	1	AE017031	AE017031 Bacillus
c 21	310.5	31.2	288404	1	AE017272	AE017272 Bacillus
c 22	303.5	30.5	304262	1	AE017005	AE017005 Bacillus
c 23	293	29.4	23738	2	AC020828	AC020828 Mus muscu
24	277.5	27.9	14140	1	AB015670	AB015670 Bacillus
25	272.5	27.4	618	12	AY657639	AY657639 Synthetic
c 26	272.5	27.4	11869	1	AE004657	AE004657 Pseudomon
c 27	262.5	26.4	301214	1	AE016786	AE016786 Pseudomon
28	260	26.1	372	6	AR388768	AR388768 Sequence
c 29	258.5	26.0	310029	1	AE016868	AE016868 Pseudomon
30	256	25.7	349287	1	BX571860	BX571860 Photorhab
c 31	256	25.7	349980	6	AX770907	AX770907 Sequence
32	250.5	25.2	636	6	AR386542	AR386542 Sequence
33	244	24.5	343529	1	CR378676	CR378676 Photobact
34	237.5	23.8	14305	1	AE014000	AE014000 Yersinia
c 35	237.5	23.8	110000	1	BX950851_45	Continuation (46 o
36	237.5	23.8	288050	1	AJ414141	AJ414141 Yersinia
37	237.5	23.8	290029	1	AE017127	AE017127 Yersinia
38	236	23.7	573	6	AX432019	AX432019 Sequence
39	236	23.7	344805	1	BX640434	BX640434 Bordetell
40	236	23.7	346287	1	BX640450	BX640450 Bordetell
c 41	235.5	23.6	294800	1	SME591789	AL591789 Sinorhizo
42	232.5	23.3	639	6	AR375589	AR375589 Sequence
c 43	232.5	23.3	302650	1	AP005958	AP005958 Bradyrhiz

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 08:56:05 ; Search time 484 Seconds
(without alignments)
2114.953 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134449_8990/app_query.fasta_1.39
1

-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487_@CGN_1_1_470_@runat_29122004_134449_8990 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*

11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	996	100.0	588	3	AAA52690	Livshits PD 7/00 Aaa52690 Escherich
2	996	100.0	750	12	ADK66005	Adk66005 E coli yf
3	684	68.7	618	11	ACH99695	App1 vaccine - too new Ach99695 Klebsiell
4	505	50.7	1668	5	AAS81979	X Aas81979 DNA encod
5	272.5	27.4	750	11	ABD10542	Abd10542 Pseudomon
c 6	262.5	26.4	5040	12	ADQ07624	Adq07624 DNA seque
7	260	26.1	372	11	ACH99702	Ach99702 Klebsiell
8	256	25.7	609	10	ACF70009	Acf70009 Photorhab
c 9	256	25.7	110000	10	ACF65385_1	Continuation (2 of
c 10	256	25.7	110000	10	ACF67367_30	Continuation (31 o
11	250.5	25.2	636	11	ACH97476	Ach97476 Klebsiell
12	236	23.7	573	6	ABK73143	Abk73143 Bacillus
13	232.5	23.3	639	10	ADF00310	Adf00310 Bacterial
14	228.5	22.9	636	10	ADF02251	Adf02251 Bacterial
15	191.5	19.2	717	9	ADA31709	Ada31709 DNA encod
16	178	17.9	726	9	ADA31746	Ada31746 DNA encod
17	173	17.4	816	11	ABD17280	Abd17280 Pseudomon
18	165	16.6	100	8	ACD79725	Acd79725 E. coli K
19	165	16.6	100	8	ACD79727	Acd79727 E. coli K
20	163.5	16.4	708	9	ADA32836	Ada32836 DNA encod
21	162	16.3	645	11	ACH95100	Ach95100 Klebsiell
22	161.5	16.2	618	8	ACA36103	Aca36103 Prokaryot
23	158.5	15.9	621	11	ABD03571	Abd03571 Pseudomon
24	158.5	15.9	633	8	ACA43829	Aca43829 Prokaryot
c 25	158.5	15.9	813	11	ABD03188	Abd03188 Pseudomon
26	157.5	15.8	618	8	ACA32157	Aca32157 Prokaryot
27	157.5	15.8	622	5	AAS93395	Aas93395 DNA encod
28	157	15.8	100	8	ACD79726	Acd79726 E. coli K
29	156.5	15.7	621	8	ACA53970	Aca53970 Prokaryot
30	156.5	15.7	621	8	ACA51728	Aca51728 Prokaryot
31	156	15.7	663	9	ADA29490	Ada29490 DNA encod
32	155.5	15.6	645	9	ADA30612	Ada30612 DNA encod
33	155.5	15.6	714	11	ABD12000	Abd12000 Pseudomon
c 34	155.5	15.6	816	11	ABD11645	Abd11645 Pseudomon
35	154	15.5	633	9	ADA31395	Ada31395 DNA encod
36	153.5	15.4	636	11	ABD05572	Abd05572 Pseudomon
c 37	153.5	15.4	1071	11	ABD05828	Abd05828 Pseudomon
38	153.5	15.4	2553	11	ABD05716	Abd05716 Pseudomon
39	153	15.4	623	8	ACA48809	Aca48809 Prokaryot
40	153	15.4	645	11	ACH96827	Ach96827 Klebsiell
41	151.5	15.2	633	8	ACA23772	Aca23772 Prokaryot
42	149.5	15.0	753	10	ADF00030	Adf00030 Bacterial
43	148	14.9	636	11	ACH96642	Ach96642 Klebsiell
44	146	14.7	669	9	ADA31058	Ada31058 DNA encod
45	143.5	14.4	639	3	AAA52689	Aaa52689 Escherich

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 09:06:26 ; Search time 95 Seconds
(without alignments)
1458.988 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134450_9044/app_query.fasta_1.39
1

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10620487 @CGN_1_1_69 @runat_29122004_134450_9044 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	684	68.7	618	4	US-09-489-039A-5490	Sequence 5490, Ap	
2	272.5	27.4	750	4	US-09-252-991A-9146	Sequence 9146, Ap	
3	260	26.1	372	4	US-09-489-039A-5497	Sequence 5497, Ap	
4	250.5	25.2	636	4	US-09-489-039A-3271	Sequence 3271, Ap	
5	232.5	23.3	639	4	US-09-543-681A-595	Sequence 595, App	
6	228.5	22.9	636	4	US-09-543-681A-2536	Sequence 2536, Ap	
7	191.5	19.2	717	4	US-09-328-352-2996	Sequence 2996, Ap	
8	178	17.9	726	4	US-09-328-352-3033	Sequence 3033, Ap	
9	173	17.4	816	4	US-09-252-991A-15884	Sequence 15884, A	
10	163.5	16.4	708	4	US-09-328-352-4123	Sequence 4123, Ap	
11	162	16.3	645	4	US-09-489-039A-895	Sequence 895, App	
12	158.5	15.9	621	4	US-09-252-991A-2175	Sequence 2175, Ap	
c 13	158.5	15.9	813	4	US-09-252-991A-1792	Sequence 1792, Ap	
14	156	15.7	663	4	US-09-328-352-777	Sequence 777, App	
15	155.5	15.6	645	4	US-09-328-352-1899	Sequence 1899, Ap	
16	155.5	15.6	714	4	US-09-252-991A-10604	Sequence 10604, A	
c 17	155.5	15.6	816	4	US-09-252-991A-10249	Sequence 10249, A	
18	154	15.5	633	4	US-09-328-352-2682	Sequence 2682, Ap	
19	153.5	15.4	636	4	US-09-252-991A-4176	Sequence 4176, Ap	
c 20	153.5	15.4	1071	4	US-09-252-991A-4432	Sequence 4432, Ap	
21	153.5	15.4	2553	4	US-09-252-991A-4320	Sequence 4320, Ap	
22	153	15.4	645	4	US-09-489-039A-2622	Sequence 2622, Ap	
23	149.5	15.0	753	4	US-09-543-681A-315	Sequence 315, App	
24	148	14.9	636	4	US-09-489-039A-2437	Sequence 2437, Ap	
25	146	14.7	669	4	US-09-328-352-2345	Sequence 2345, Ap	
26	138.5	13.9	660	4	US-09-489-039A-560	Sequence 560, App	
c 27	137	13.8	269223	4	US-09-596-002-41	Sequence 41, Appl	
28	132	13.3	489	4	US-09-252-991A-15914	Sequence 15914, A	
29	132	13.3	627	4	US-09-328-352-985	Sequence 985, App	
30	128.5	12.9	687	4	US-09-543-681A-682	Sequence 682, App	
31	128.5	12.9	723	4	US-09-328-352-3411	Sequence 3411, Ap	
32	128.5	12.9	1200	3	US-09-396-357-1	Sequence 1, Appli	
33	128	12.9	663	4	US-09-543-681A-373	Sequence 373, App	
34	127	12.8	603	4	US-09-328-352-647	Sequence 647, App	
35	125.5	12.6	645	4	US-09-328-352-2569	Sequence 2569, Ap	
36	123.5	12.4	687	4	US-09-252-991A-7266	Sequence 7266, Ap	
37	123.5	12.4	834	4	US-09-252-991A-6447	Sequence 6447, Ap	
c 38	123.5	12.4	1521	4	US-09-252-991A-7437	Sequence 7437, Ap	
39	123.5	12.4	2397	4	US-09-252-991A-7203	Sequence 7203, Ap	
40	122.5	12.3	606	4	US-09-328-352-2283	Sequence 2283, Ap	
c 41	121	12.1	930	4	US-09-252-991A-6103	Sequence 6103, Ap	
42	115.5	11.6	783	4	US-09-252-991A-9421	Sequence 9421, Ap	
43	115.5	11.6	1596	4	US-09-252-991A-9478	Sequence 9478, Ap	
c 44	115.5	11.6	1650	4	US-09-252-991A-9352	Sequence 9352, Ap	
45	112.5	11.3	750	4	US-09-328-352-1687	Sequence 1687, Ap	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 09:05:27 ; Search time 531 Seconds
(without alignments)
2074.218 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134450_9020/app_query.fasta_1.39
1

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10620487_@CGN_1_1_480_@runat_29122004_134450_9020
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

```

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query						
No.	Score	Match	Length	DB	ID		Description		
	1	996	100.0	750	16	US-10-620-487-1	<i>Appl</i>	Sequence 1, Appli	
	2	236	23.7	573	9	US-09-974-300-434		Sequence 434, App	
	3	161.5	16.2	618	16	US-10-282-122A-23973		Sequence 23973, A	
	4	158.5	15.9	633	16	US-10-282-122A-31699		Sequence 31699, A	
	5	157.5	15.8	618	16	US-10-282-122A-20027		Sequence 20027, A	
	6	156.5	15.7	621	16	US-10-282-122A-39598		Sequence 39598, A	
	7	156.5	15.7	621	16	US-10-282-122A-41840		Sequence 41840, A	
	8	153	15.4	623	16	US-10-282-122A-36679		Sequence 36679, A	
	9	151.5	15.2	633	16	US-10-282-122A-11642		Sequence 11642, A	
	10	142	14.3	651	15	US-10-156-761-3368		Sequence 3368, Ap	
c	11	142	14.3	9025608	15	US-10-156-761-1		Sequence 1, Appli	
	12	137.5	13.8	618	16	US-10-282-122A-40780		Sequence 40780, A	
c	13	137	13.8	269223	16	US-10-672-787-41		Sequence 41, Appl	
	14	129.5	13.0	543	16	US-10-282-122A-8689		Sequence 8689, Ap	
	15	128.5	12.9	1200	9	US-09-927-395-1		Sequence 1, Appli	
	16	128.5	12.9	1200	9	US-09-847-392-1		Sequence 1, Appli	
	17	123.5	12.4	630	16	US-10-282-122A-30630		Sequence 30630, A	
	18	123	12.3	2731748	17	US-10-297-465A-1		Sequence 1, Appli	
	19	118.5	11.9	792	10	US-09-746-660A-13		Sequence 13, Appl	
c	20	118.5	11.9	3309400	9	US-09-738-626-1		Sequence 1, Appli	
	21	117.5	11.8	630	16	US-10-282-122A-33154		Sequence 33154, A	
	22	116.5	11.7	669	9	US-09-738-626-2570		Sequence 2570, Ap	
	23	112	11.2	621	9	US-09-738-626-2918		Sequence 2918, Ap	
c	24	112	11.2	85692	16	US-10-461-194-1		Sequence 1, Appli	
c	25	111	11.1	86941	16	US-10-461-194-2		Sequence 2, Appli	
	26	110.5	11.1	615	15	US-10-156-761-3747		Sequence 3747, Ap	
	27	109.5	11.0	627	16	US-10-282-122A-14918		Sequence 14918, A	
	28	108	10.8	3309400	9	US-09-738-626-1		Sequence 1, Appli	
	29	107.5	10.8	672	15	US-10-156-761-246		Sequence 246, App	
c	30	106.5	10.7	2731748	17	US-10-297-465A-1		Sequence 1, Appli	
	31	104.5	10.5	1830121	14	US-10-329-960-1		Sequence 1, Appli	
	32	104.5	10.5	1830121	16	US-10-329-670-1		Sequence 1, Appli	
	33	104.5	10.5	1830121	18	US-10-158-865-1		Sequence 1, Appli	
	34	104	10.4	678	9	US-09-738-626-165		Sequence 165, App	
	35	98.5	9.9	417	15	US-10-287-274-274		Sequence 274, App	
	36	98.5	9.9	417	16	US-10-282-122A-6496		Sequence 6496, Ap	

	37	96	9.6	853	17	US-10-767-795-5271	Sequence 5271, Ap
	38	96	9.6	2847	17	US-10-437-963-58805	Sequence 58805, A
	39	95.5	9.6	1419	16	US-10-282-122A-25105	Sequence 25105, A
	40	95	9.5	1611	16	US-10-282-122A-31927	Sequence 31927, A
c	41	95	9.5	6357	18	US-10-859-149-2	Sequence 2, Appli
c	42	95	9.5	1163020	16	US-10-398-221-10	Sequence 10, Appl
c	43	95	9.5	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
	44	94	9.4	1881	15	US-10-369-493-27537	Sequence 27537, A
	45	93.5	9.4	822	10	US-09-746-660A-51	Sequence 51, Appl

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OM protein - protein search, using sw model

Run on: January 3, 2005, 08:48:36 ; Search time 24 Seconds
(without alignments)
781.761 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	993	99.7	195	2	A65036	hypothetical 21.2
2	979	98.3	195	2	D91059	hypothetical prote
3	979	98.3	195	2	B85904	hypothetical prote
4	884	88.8	195	2	AF0830	probable membrane
5	272.5	27.4	205	2	B83356	conserved hypothet
6	235.5	23.6	200	2	AI0022	probable ABC-trans
7	172	17.3	204	2	B82166	conserved hypothet
8	169	17.0	222	2	E87264	efflux protein, Ly
9	165.5	16.6	206	2	B91223	homoserine/homoser
10	164	16.5	205	2	AI2614	RhtB family transp
11	164	16.5	224	2	H97396	dihydrodipicolinat
12	163	16.4	210	2	E87252	efflux protein, Ly
13	162.5	16.3	249	2	AG3485	homoserine/homoser

14	160.5	16.1	222	2	F82353	conserved hypothet
15	158.5	15.9	197	2	B83280	hypothetical prote
16	158.5	15.9	216	2	C55580	hypothetical prote
17	158	15.9	210	2	D84016	hypothetical prote
18	156.5	15.7	206	2	AF0917	homoserine/homoser
19	156.5	15.7	206	2	AG0466	probable homoserin
20	156.5	15.7	235	2	AD2904	RhtB family transp
21	156.5	15.7	235	2	F97679	hypothetical prote
22	155.5	15.6	209	2	E82388	conserved hypothet
23	155.5	15.6	216	2	F83051	conserved hypothet
24	154.5	15.5	207	2	D83187	hypothetical prote
25	153	15.4	212	2	H87498	LysE family transl
26	143.5	14.4	212	2	F64940	hypothetical prote
27	143	14.4	212	2	AF2805	homoserine/homoser
28	143	14.4	273	2	F97584	hypothetical prote
29	142.5	14.3	212	2	G85790	hypothetical prote
30	140.5	14.1	212	2	C90942	hypothetical prote
31	139	14.0	212	2	AD0714	probable membrane
32	137.5	13.8	205	2	G82358	conserved hypothet
33	135.5	13.6	278	2	E98301	hypothetical prote
34	134.5	13.5	210	2	AC2982	RhtB family transp
35	130	13.1	207	2	E83703	hypothetical prote
36	129	13.0	208	2	C82471	conserved hypothet
37	123.5	12.4	206	2	C82979	hypothetical prote
38	123.5	12.4	209	2	C82990	hypothetical prote
39	123	12.3	213	2	C82523	amino acid transpo
40	122.5	12.3	205	2	AH3641	transporter, lysE
41	122	12.2	206	2	C82139	conserved hypothet
42	122	12.2	216	2	A97675	amino acid efflux-
43	120	12.0	208	2	G87305	efflux protein, Ly
44	119.5	12.0	204	2	B82410	conserved hypothet
45	119.5	12.0	208	2	G84086	dihydrodipicolinat

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 3, 2005, 08:57:56 ; Search time 3043 Seconds
(without alignments)
2335.113 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLLSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10620487/runat_29122004_134449_9010/app_query.fasta_1.39
1

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=US10620487_@CGN_1_1_3437_@runat_29122004_134449_9010 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	617	61.9	681	6	CA366654	CA366654 642278 NC
	2	501	50.3	856	9	CL650636	CL650636 PRI0110a_
	3	464	46.6	791	9	CL688782	CL688782 PRI014b_G
	4	451	45.3	736	9	CL688905	CL688905 PRI014d_C
c	5	311.5	31.3	819	8	BH447440	BH447440 BOHQB49TF
c	6	219.5	22.0	862	9	CL666889	CL666889 PRI0153c_
	7	217	21.8	420	8	BH374397	BH374397 AG-ND-180
c	8	202.5	20.3	1233	8	BZ579504	BZ579504 msh2_6385
	9	200	20.1	450	8	BH379453	BH379453 AG-ND-163
c	10	199	20.0	118	6	CA374430	CA374430 648800 NC
c	11	198.5	19.9	511	6	CD093163	CD093163 MC1-0105T
c	12	165.5	16.6	665	9	AG613339	AG613339 Escherich
	13	165.5	16.6	818	9	CL669909	CL669909 PRI0160c_
c	14	162.5	16.3	863	9	CL689879	CL689879 PRI0152b_
c	15	149	15.0	784	8	BZ577923	BZ577923 msh2_5638
c	16	137.5	13.8	1018	8	BZ561476	BZ561476 pacs2-164
	17	121.5	12.2	770	8	BZ573390	BZ573390 msh2_3082
	18	120	12.0	237	2	AW802587	AW802587 IL5-UM007
	19	115.5	11.6	443	4	BG038404	BG038404 dg34h08.y
c	20	111.5	11.2	798	9	CNS01QYA	AL156722 Anopheles
c	21	110.5	11.1	407	8	AZ576789	AZ576789 01a12 Sho
	22	110.5	11.1	428	2	BF614897	BF614897 dg18a02.y
c	23	109	10.9	829	8	BZ549776	BZ549776 pacs1-60_
c	24	108	10.8	1014	8	BZ558389	BZ558389 pacs1-60_
c	25	106	10.6	799	7	CN823350	CN823350 Oa_splbn_
c	26	105	10.5	1244	2	BF981306	BF981306 602308552
	27	101.5	10.2	881	8	BZ549402	BZ549402 pacs1-60_
	28	101	10.1	1239	8	BZ555841	BZ555841 pacs1-60_
	29	101	10.1	1932	9	CG756745	CG756745 P051-4-F0
c	30	100	10.0	1299	2	BE966761	BE966761 601661261
c	31	99.5	10.0	774	5	BU961093	BU961093 AGENCOURT
c	32	99.5	10.0	1012	9	CL119129	CL119129 ISB1-75N6
c	33	99.5	10.0	1068	9	AG078894	AG078894 Pan trogl
	34	99	9.9	614	7	CO536048	CO536048 tail0f08.
	35	98	9.8	562	8	AQ365906	AQ365906 nbxb0064N
c	36	98	9.8	1151	2	BF037237	BF037237 601460948
c	37	97	9.7	1112	4	BI763871	BI763871 603049636
c	38	97	9.7	1690	2	BF128393	BF128393 601810283
c	39	97	9.7	1823	4	BG253780	BG253780 602366662
c	40	95.5	9.6	621	8	AZ452242	AZ452242 1M0252D04
	41	95.5	9.6	641	7	CN222730	CN222730 RJA088F06
c	42	95.5	9.6	649	8	AZ649701	AZ649701 1M0519P23
c	43	95.5	9.6	1623	2	BF131641	BF131641 601820464
c	44	95	9.5	1745	9	CL512730	CL512730 SAIL_866_
c	45	94.5	9.5	723	4	BJ502772	BJ502772 BJ502772

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OM protein - protein search, using sw model

Run on: January 3, 2005, 07:58:40 ; Search time 106 Seconds
(without alignments)
1058.472 Million cell updates/sec

Title: US-10-620-487-2
Perfect score: 996
Sequence: 1 VTPTLTSAFWTYTLITAMTP.....RQLNIVLALLLVYCAVRIFY 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	993	99.7	195	1 YFIK_ECOLI	P38101 escherichia
2	989	99.3	195	2 Q8FF11	Q8ff11 escherichia
3	987	99.1	195	2 Q7C0E0	Q7c0e0 shigella fl
4	987	99.1	195	2 Q83K22	Q83k22 shigella fl
5	979	98.3	195	2 Q7ABJ3	Q7abj3 escherichia
6	979	98.3	195	2 Q8XA19	Q8xa19 escherichia
7	884	88.8	195	2 Q8Z4J7	Q8z4j7 salmonella
8	884	88.8	195	2 Q8ZMX5	Q8zmx5 salmonella
9	367.5	36.9	200	2 Q7P2H4	Q7p2h4 fusobacteri
10	311.5	31.3	194	2 Q6HIR1	Q6hir1 bacillus th
11	311.5	31.3	194	2 Q81QH8	Q81qh8 bacillus an
12	311.5	31.3	194	2 AAT31562	Aat31562 bacillus
13	310.5	31.2	194	2 Q738B5	Q738b5 bacillus ce
14	310.5	31.2	194	2 AAS41397	Aas41397 bacillus
15	303.5	30.5	194	2 Q81DI7	Q81di7 bacillus ce

16	277.5	27.9	198	2	O82971	O82971 bacillus sp
17	272.5	27.4	205	2	Q9I1G9	Q9ilg9 pseudomonas
18	262.5	26.4	209	2	Q88HF4	Q88hf4 pseudomonas
19	258.5	26.0	202	2	Q87ZH7	Q87zh7 pseudomonas
20	256	25.7	202	2	Q7N9E0	Q7n9e0 photorhabdu
21	244	24.5	204	2	Q6LKF4	Q6lkf4 photobacter
22	244	24.5	204	2	CAG22196	Cag22196 photobact
23	237.5	23.8	200	2	Q6CZU2	Q6czu2 erwinia car
24	236	23.7	219	2	Q7W450	Q7w450 bordetella
25	236	23.7	219	2	Q7WFK7	Q7wfk7 bordetella
26	235.5	23.6	197	2	Q92NS0	Q92ns0 rhizobium m
27	235.5	23.6	200	2	Q8ZJD2	Q8zjd2 yersinia pe
28	234.5	23.5	192	2	Q8CK91	Q8ck91 yersinia pe
29	234.5	23.5	192	2	AAS60457	Aas60457 yersinia
30	232.5	23.3	202	2	Q89G49	Q89g49 bradyrhizob
31	232	23.3	219	2	Q7VSL5	Q7vsl5 bordetella
32	231	23.2	196	2	Q7QMF4	Q7qmf4 anopheles g
33	222.5	22.3	197	2	Q8EG90	Q8eg90 shewanella
34	221	22.2	193	2	Q88HC2	Q88hc2 pseudomonas
35	215.5	21.6	199	2	Q8D574	Q8d574 vibrio vuln
36	214.5	21.5	188	2	Q882W8	Q882w8 pseudomonas
37	213.5	21.4	198	2	Q98KK8	Q98kk8 rhizobium l
38	211.5	21.2	200	2	Q6LVD7	Q6lvd7 photobacter
39	211.5	21.2	200	2	CAG18738	Cag18738 photobact
40	211.5	21.2	206	2	Q7NWS8	Q7nws8 chromobacte
41	206.5	20.7	208	2	Q7NWP5	Q7nwp5 chromobacte
42	206	20.7	195	2	Q7MG87	Q7mg87 vibrio vuln
43	204.5	20.5	248	2	Q7WDP6	Q7wdp6 bordetella
44	202	20.3	195	2	Q8D4N7	Q8d4n7 vibrio vuln
45	199.5	20.0	208	2	Q7W2P8	Q7w2p8 bordetella